--71. A method for identification of a nucleic acid molecule that modulates a process in a biological system comprising the steps of:

a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and

b) determining the nucleotide sequence of at least a portion of the substrate binding domain of said nucleic acid catalyst from said biological system in which the process has been modulated.

72. A method for identifying one or more nucleic acid molecules involved in a process in a biological system comprising the steps of:

a) providing a library of a nucleic acid catalyst, with a substrate binding domain and a catalytic domain, wherein said substrate binding domain comprises a random sequence, to said biological system under conditions suitable for said process to be altered;

b) identifying any said nucleic acid catalyst present in said biological system where said process has been altered; and

c) determining the nucleotide sequence of at least a portion of the binding domain of said any said nucleic acid catalyst to allow said identification of said nucleic acid molecule involved in said process in said biological system.

73. A method for identification of a nucleic acid catalyst that modulates a process in a biological system comprising the steps of:

a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and

b) identifying said nucleic acid catalyst from said biological system in which the process has been modulated.

74. The method of any of claims 71-73, wherein said biological system is a bacterial cell.

75. The method of any of claims 71-73, wherein said biological system is of plant origin.

76. The method of any of claims 71-73, wherein said biological system is of mammalian origin.

77. The method of any of claims 71-73, wherein said nucleic acid catalyst is in a hammerhead motif.

78. The method of any of claims 71-73, wherein said nucleic acid catalyst is in a hairpin motif.

79. The method of any of claims 71-73, wherein said nucleic acid catalyst is in a group I intron ribozyme motif, group II intron ribozyme motif, VS ribozyme motif or RNase P ribozyme motif.

80. The method of any of claims 71-73, wherein said process is selected from the group consisting of growth, proliferation, apoptosis, morphology, angiogenesis, differentiation, migration, viral multiplication, drug resistance, signal transduction, cell cycle regulation, temperature sensitivity and chemical sensitivity.

81. The method of any of claims 71-73, wherein said random library of nucleic acid catalysts is encoded by an expression vector in a manner which allows expression of said nucleic acid catalysts.

82. The method of claim 81, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) a sequence encoding at least one said nucleic acid catalyst; and

wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

83. The method of claim 81, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an open reading frame for a polypeptide;

d) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; and

wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

84. The method of claim 81, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) a sequence encoding at least one said nucleic acid catalyst; and

wherein said sequence is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

85. The method of claim 81, wherein said expression vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) an open reading frame for a polypeptide;

e) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

86. The method of claim 81, wherein said expression vector is derived from a retrovirus.

87. The method of claim 81, wherein said expression vector is derived from an adenovirus.

88. The method of claim 81, wherein said expression vector is derived from an adeno-associated virus.

89. The method of claim 81, wherein said expression vector is derived from an alphavirus.

90. The method of claim 81, wherein said expression vector is derived from a bacterial plasmid.

91. The method of claim 81, wherein said expression vector is operably linked to a RNA polymerase II promoter element.

92. The method of claim 81, wherein said expression vector is operably linked to a RNA polymerase III promoter element.

93. The method of claim 92, wherein said RNA polymerase III promoter is derived from a transfer RNA gene.

94. The method of any of claims 71-73, wherein said biological system is of an eukaryotic origin.

95. The method of any of claims 71-73, wherein said biological system is of a prokaryotic origin.

96. The method of any of claims 71-73, wherein said substrate binding domain is of length between 12 and 100 nucleotides.

97. The method of any of claims 71-73, wherein said substrate binding domain is of length between 14 and 24 nucleotides.

98. The method of any of claims 71-73, wherein said nucleic acid catalyst comprises two substrate binding arms.

99. The method of claim 98, wherein said substrate binding arms are of similar length.

100. The method of claim 98, wherein said substrate binding arms are of different length.--

REMARKS

The Invention.

This invention is the application of catalytic nucleic acid (ribozymes) to effect a phenotypic change in a cell.